

## SEQUENCE LISTING

<110> Roch, Jean-Marc  
Bartel, Paul L.  
Heichman, Karen

<120> Protein-Protein Interactions in Neurodegenerative  
Diseases

<130> Protein Interactions in ND

<140>  
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<150> US 60/240,790  
<151> 2000-10-17

<160> 4

<170> PatentIn Ver. 2.0

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<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence:tail for  
forward primer for yeast two-hybrid system

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<212> DNA  
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reverse primer for yeast two-hybrid system

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taataaaaac atttttcagg gacgttagcca tccagagaca ttccattatt gttccattga 180  
cctttccctc atcactgagt cctttggagc tgagtt atg tca aca gct gcc tta 234

Met Ser Thr Ala Ala Leu		
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att act ttg gtc aga agt ggt ggg aac cag gtg aga agg aga gtg ctg	282	
Ile Thr Leu Val Arg Ser Gly Gly Asn Gln Val Arg Arg Arg Val Leu		
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cta agc tcc cgc ctg ctg cag gac gac agg cgg gtg aca ccc acg tgc	330	
Leu Ser Ser Arg Leu Leu Gln Asp Asp Arg Arg Val Thr Pro Thr Cys		
25 30 35		
cac agc tcc act tca gag cct agg tgt tct cgg ttt gac cca gat ggt	378	
His Ser Ser Thr Ser Glu Pro Arg Cys Ser Arg Phe Asp Pro Asp Gly		
40 45 50		
agt ggg agt cca gct acc tgg gac aat ttt ggg atc tgg gat aac cgc	426	
Ser Gly Ser Pro Ala Thr Trp Asp Asn Phe Gly Ile Trp Asp Asn Arg		
55 60 65 70		
att gat gag cca att ctg ctg cca ccc agc att aag tat ggc aag cca	474	
Ile Asp Glu Pro Ile Leu Leu Pro Pro Ser Ile Lys Tyr Gly Lys Pro		
75 80 85		
att ccc aaa atc agc ttg gaa aat gtg ggg tgc gcc tca cag att ggc	522	
Ile Pro Lys Ile Ser Leu Glu Asn Val Gly Cys Ala Ser Gln Ile Gly		
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Lys Arg Lys Glu Asn Glu Asp Arg Phe Asp Phe Ala Gln Leu Thr Asp		
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gag gtc ctg tac ttt gca gtg tat gat gga cac ggt gga cct gca gca	618	
Glu Val Leu Tyr Phe Ala Val Tyr Asp Gly His Gly Gly Pro Ala Ala		
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gct gat ttc tgt cat acc cac atg gag aaa tgt att atg gat ttg ctt	666	
Ala Asp Phe Cys His Thr His Met Glu Lys Cys Ile Met Asp Leu Leu		
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cct aag gag aag aac ttg gaa act ctg ttg acc ttg gct ttt cta gaa	714	
Pro Lys Glu Lys Asn Leu Glu Thr Leu Leu Thr Leu Ala Phe Leu Glu		
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ctt ctg acc tct ggg act act gca aca gta gcc cta ttg cga gat ggt	810	
Leu Leu Thr Ser Gly Thr Ala Thr Val Ala Leu Leu Arg Asp Gly		
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Arg Lys Gly Lys Pro Met Lys Leu Thr Ile Asp His Thr Pro Glu Arg		
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Ser Ile Gly Asp Leu Asp Leu Lys Thr Ser Gly Val Ile Ala Glu Pro			
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Leu Thr Thr Asp Gly Ile Asn Phe Met Val Asn Ser Gln Glu Ile Cys			
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Val Val Pro Phe Gly Ala Trp Gly Lys Tyr Lys Asn Ser Glu Ile Asn			
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 35 40 45  
 Arg Phe Asp Pro Asp Gly Ser Gly Ser Pro Ala Thr Trp Asp Asn Phe  
 50 55 60  
 Gly Ile Trp Asp Asn Arg Ile Asp Glu Pro Ile Leu Leu Pro Pro Ser  
 65 70 75 80  
 Ile Lys Tyr Gly Lys Pro Ile Pro Lys Ile Ser Leu Glu Asn Val Gly  
 85 90 95  
 Cys Ala Ser Gln Ile Gly Lys Arg Lys Glu Asn Glu Asp Arg Phe Asp  
 100 105 110  
 Phe Ala Gln Leu Thr Asp Glu Val Leu Tyr Phe Ala Val Tyr Asp Gly  
 115 120 125  
 His Gly Gly Pro Ala Ala Asp Phe Cys His Thr His Met Glu Lys  
 130 135 140  
 Cys Ile Met Asp Leu Leu Pro Lys Glu Lys Asn Leu Glu Thr Leu Leu  
 145 150 155 160  
 Thr Leu Ala Phe Leu Glu Ile Asp Lys Ala Phe Ser Ser His Ala Arg  
 165 170 175  
 Leu Ser Ala Asp Ala Thr Leu Leu Thr Ser Gly Thr Thr Ala Thr Val  
 180 185 190  
 Ala Leu Leu Arg Asp Gly Ile Glu Leu Val Val Ala Ser Val Gly Asp  
 195 200 205  
 Ser Arg Ala Ile Leu Cys Arg Lys Gly Lys Pro Met Lys Leu Thr Ile  
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Asp His Thr Pro Glu Arg Lys Asp Glu Lys Glu Arg Ile Lys Lys Cys  
225 230 235 240

Gly Gly Phe Val Ala Trp Asn Ser Leu Gly Gln Pro His Val Asn Gly  
245 250 255

Arg Leu Ala Met Thr Arg Ser Ile Gly Asp Leu Asp Leu Lys Thr Ser  
260 265 270

Gly Val Ile Ala Glu Pro Glu Thr Lys Arg Ile Lys Leu His His Ala  
275 280 285

Asp Asp Ser Phe Leu Val Leu Thr Thr Asp Gly Ile Asn Phe Met Val  
290 295 300

Asn Ser Gln Glu Ile Cys Asp Phe Val Asn Gln Cys His Asp Pro Asn  
305 310 315 320

Glu Ala Ala His Ala Val Thr Glu Gln Ala Ile Gln Tyr Gly Thr Glu  
325 330 335

Asp Asn Ser Thr Ala Val Val Val Pro Phe Gly Ala Trp Gly Lys Tyr  
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Lys Asn Ser Glu Ile Asn Phe Ser Phe Ser Arg Ser Phe Ala Ser Ser  
355 360 365

Gly Arg Trp Ala  
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